5620

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,447

Source: PCT

Date Processed by STIC: 1-12-06

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PCT

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        RAW SEQUENCE LISTING                      DATE: 01/12/2005
        PATENT APPLICATION:  US/10/519,447        TIME: 16:15:44

        Input Set : A:\Q85576 Sequence Listing.txt
        Output Set: N:\CRF4\01122005\J519447.raw

  3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
  4        Makoto OGINO
  5        Hideki ENDOH
  7 <120> TITLE OF INVENTION: METHOD FOR SCREENING AN AGENT FOR IMPROVING INSULIN
RESISTANCE
  9 <130> FILE REFERENCE: Q85576
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/519,447
C--> 11 <141> CURRENT FILING DATE: 2004-12-30
  11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/08367
  12 <151> PRIOR FILING DATE: 2003-07-01
  14 <150> PRIOR APPLICATION NUMBER: JP 2002-193814
  15 <151> PRIOR FILING DATE: 2002-07-02
  17 <160> NUMBER OF SEQ ID NOS: 16
  19 <170> SOFTWARE: PatentIn version 3.1
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 1845
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Homo sapiens
  26 <220> FEATURE:
  27 <221> NAME/KEY: CDS
  28 <222> LOCATION: (1)..(1845)
  29 <223> OTHER INFORMATION:
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  33 atg tcg ggt tat tcg agt gac cga gac cgc ggc cgg gac cga ggg ttt        48
  34 Met Ser Gly Tyr Ser Ser Asp Arg Asp Arg Gly Arg Asp Arg Gly Phe
  35 1               5               10                  15
  37 ggt gca cct cga ttt gga gga agt agg gca ggg ccc tta tct gga aag        96
  38 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
  39             20                  25                  30
  41 aag ttt gga aac cct ggg gag aaa tta gtt aaa aag aag tgg aat ctt        144
  42 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Lys Trp Asn Leu
  43         35                  40                  45
  45 gat gag ctg cct aaa ttt gag aag aat ttt tat caa gag cac cct gat        192
  46 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
  47     50                  55                  60
  49 ttg gct agg cgc aca gca caa gag gtg gaa aca tac aga aga agc aag        240
  50 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
  51 65                  70                  75                  80
  53 gaa att aca gtt aga ggt cac aac tgc ccg aag cca gtt cta aat ttt        288
  54 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
  55                 85                  90                  95
  57 tat gaa gcc aat ttc cct gca aat gtc atg gat gtt att gca aga cag        336
  58 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
  59                 100                 105                 110
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 61 aat ttc act gaa ccc act gct att caa gct cag gga tgg cca gtt gct      384
 62 Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala      ---
 63         115                 120                 125
 65 cta agt gga ttg gat atg gtt gga gtg gca cag act gga tct ggg aaa      432
 66 Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys
 67     130                 135                 140
 69 aca ttg tct tat ttg ctt cct gcc att gtc cac atc aat cat cag cca      480
 70 Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro
 71 145                 150                 155                 160
 73 ttc cta gag aga ggc gat ggg cct att tgt ttg gtg ctg gca cca act      528
 74 Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr
 75                 165                 170                 175
 77 cgg gaa ctg gcc caa cag gtg cag caa gta gct gct gaa tat tgt aga      576
 78 Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg
 79             180                 185                 190
 81 gca tgt cgc ttg aag tct act tgt atc tac ggt ggt gct cct aag gga      624
 82 Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly
 83         195                 200                 205
 85 cca caa ata cgt gat ttg gag aga ggt gtg gaa atc tgt att gca aca      672
 86 Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr
 87     210                 215                 220
 89 cct gga aga ctg att gac ttt tta gag tgt gga aaa acc aat ctg aga      720
 90 Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg
 91 225                 230                 235                 240
 93 aga aca acc tac ctt gtc ctt gat gaa gca gat aga atg ctt gat atg      768
 94 Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met
 95                 245                 250                 255
 97 ggc ttt gaa ccc caa ata agg aag att gtg gat caa ata aga cct gat      816
 98 Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp
 99             260                 265                 270
101 agg caa act cta atg tgg agt gcg act tgg cca aaa gaa gta aga cag      864
102 Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln
103         275                 280                 285
105 ctt gct gaa gat ttc ctg aaa gac tat att cat ata aac att ggt gca      912
106 Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala
107     290                 295                 300
109 ctt gaa ctg agt gca aac cac aac att ctt cag att gtg gat gtg tgt      960
110 Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys
111 305                 310                 315                 320
113 cat gac gta gaa aag gat gaa aaa ctt att cgt cta atg gaa gag atc      1008
114 His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile
115                 325                 330                 335
117 atg agt gag aag gag aat aaa acc att gtt ttt gtg gaa acc aaa aga      1056
118 Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg
119             340                 345                 350
121 aga tgt gat gag ctt acc aga aaa atg agg aga gat ggg tgg cct gcc      1104
122 Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala
123         355                 360                 365
125 atg ggt atc cat ggt gac aag agt caa caa gag cgt gac tgg gtt cta      1152
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Input Set : A:\Q85576 Sequence Listing.txt
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126 Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu
127     370             --375--             380
129 aat gaa ttc aaa cat gga aaa gct cct att ctg att gct aca gat gtg      1200
130 Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val
131 385             390             395             400
133 gcc tcc aga ggg cta gat gtg gaa gat gtg aaa ttt gtc atc aat tat      1248
134 Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr
135             405             410             415
137 gac tac cct aac tcc tca gag gat tat att cat cga att gga aga act      1296
138 Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr
139             420             425             430
141 gct cgc agt acc aaa aca ggc aca gca tac act ttc ttt aca cct aat      1344
142 Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn
143             435             440             445
145 aac ata aag caa gtg agc gac ctt atc tct gtg ctt cgt gaa gct aat      1392
146 Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn
147     450             455             460
149 caa gca att aat ccc aag ttg ctt cag ttg gtc gaa gac aga ggt tca      1440
150 Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser
151 465             470             475             480
153 ggt cgt tcc agg ggt aga gga ggc atg aag gat gac cgt cgg gac aga      1488
154 Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg
155             485             490             495
157 tac tct gcg ggc aaa agg ggt gga ttt aat acc ttt aga gac agg gaa      1536
158 Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu
159             500             505             510
161 aat tat gac aga ggt tac tct agc ctg ctt aaa aga gat ttt ggg gca      1584
162 Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala
163             515             520             525
165 aaa act cag aat ggt gtt tac agt gct gca aat tac acc aat ggg agc      1632
166 Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser
167     530             535             540
169 ttt gga agt aat ttt gtg tct gct ggt ata cag acc agt ttt agg act      1680
170 Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr
171 545             550             555             560
173 ggt aat cca aca ggg act tac cag aat ggt tat gat agc act cag caa      1728
174 Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln
175             565             570             575
177 tac gga agt aat gtt cca aat atg cac aat ggt atg aac caa cag gca      1776
178 Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala
179             580             585             590
181 tat gca tat cct gct act gca gct gca cct atg att ggt tat cca atg      1824
182 Tyr Ala Tyr Pro Ala Thr Ala Ala Ala Pro Met Ile Gly Tyr Pro Met
183             595             600             605
185 cca aca gga tat tcc caa taa                                           1845
186 Pro Thr Gly Tyr Ser Gln
187     610
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 614
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RAW SEQUENCE LISTING   DATE: 01/12/2005
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Input Set : A:\Q85576 Sequence Listing.txt
Output Set: N:\CRF4\01122005\J519447.raw

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192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
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201 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
202             20                  25                  30
205 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Trp Asn Leu
206         35                  40                  45
209 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
210     50                  55                  60
213 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
214 65                  70                  75                  80
217 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
218                 85                  90                  95
221 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
222             100                 105                 110
225 Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala
226             115                 120                 125
229 Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys
230     130                 135                 140
233 Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro
234 145                 150                 155                 160
237 Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr
238             165                 170                 175
241 Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg
242             180                 185                 190
245 Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly
246         195                 200                 205
249 Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr
250     210                 215                 220
253 Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg
254 225                 230                 235                 240
257 Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met
258             245                 250                 255
261 Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp
262             260                 265                 270
265 Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln
266         275                 280                 285
269 Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala
270     290                 295                 300
273 Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys
274 305                 310                 315                 320
277 His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile
278             325                 330                 335
281 Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg
282             340                 345                 350
285 Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala
286         355                 360                 365
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```
289 Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu
290     370                 375             380
293 Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val
294 385                 390             395                 400
297 Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr
298             405             410             415
301 Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr
302             420             425             430
305 Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn
306         435             440             445
309 Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn
310     450             455             460
313 Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser
314 465             470                 475             480
317 Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg
318             485             490             495
321 Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu
322             500             505             510
325 Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala
326         515             520             525
329 Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser
330     530             535             540
333 Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr
334 545             550             555             560
337 Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln
338             565             570             575
341 Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala
342             580             585             590
345 Tyr Ala Tyr Pro Ala Thr Ala Ala Ala Pro Met Ile Gly Tyr Pro Met
346         595             600             605
349 Pro Thr Gly Tyr Ser Gln
350     610
353 <210> SEQ ID NO: 3
354 <211> LENGTH: 1518
355 <212> TYPE: DNA
356 <213> ORGANISM: Homo sapiens
358 <220> FEATURE:
359 <221> NAME/KEY: CDS
360 <222> LOCATION: (1)..(1518)
361 <223> OTHER INFORMATION:
363 <400> 3
364 atg ggt gaa act ctg gga gat tct cct att gac cca gaa agc gat tcc      48
365 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
366 1               5                   10                  15
368 ttc act gat aca ctg tct gca aac ata tca caa gaa atg acc atg gtt      96
369 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
370             20                  25                  30
372 gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg     144
373 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
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VERIFICATION SUMMARY   DATE: 01/12/2005
PATENT APPLICATION: US/10/519,447   TIME: 16:15:45

Input Set : A:\Q85576 Sequence Listing.txt
Output Set: N:\CRF4\01122005\J519447.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:361
L:638 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:636